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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2007; month=12; day=4; hr=12; min=27; sec=1; ms=600;]

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Application No: 10527265 Version No: 1.0

Input Set:

Output Set:

Started: 2007-11-15 10:58:06.657
Finished: 2007-11-15 10:59:11.659
Elapsed: 0 hr(s) 1 min(s) 5 sec(s) 2 ms
Total Warnings: 183
Total Errors: 0
No. of SeqIDs Defined: 1735
Actual SeqID Count: 1735

Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (235)
W 251	Found intentionally skipped sequence in SEQID (236)
W 251	Found intentionally skipped sequence in SEQID (469)
W 251	Found intentionally skipped sequence in SEQID (1295)
W 213	Artificial or Unknown found in <213> in SEQ ID (1557)
W 213	Artificial or Unknown found in <213> in SEQ ID (1558)
W 213	Artificial or Unknown found in <213> in SEQ ID (1559)
W 213	Artificial or Unknown found in <213> in SEQ ID (1560)
W 213	Artificial or Unknown found in <213> in SEQ ID (1561)
W 213	Artificial or Unknown found in <213> in SEQ ID (1562)
W 213	Artificial or Unknown found in <213> in SEQ ID (1563)
W 213	Artificial or Unknown found in <213> in SEQ ID (1564)
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W 213	Artificial or Unknown found in <213> in SEQ ID (1566)
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W 213	Artificial or Unknown found in <213> in SEQ ID (1568)
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W 213	Artificial or Unknown found in <213> in SEQ ID (1571)
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Input Set:

Output Set:

Started: 2007-11-15 10:58:06.657
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Elapsed: 0 hr(s) 1 min(s) 5 sec(s) 2 ms
Total Warnings: 183
Total Errors: 0
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Actual SeqID Count: 1735

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (1576) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Primal, Inc.
Gaitanaris, George A.
Bergmann, John E.
Gragerov, Alexander
John, Hohmann
Li, Fusheng
Madisen, Linda
McIlwain, Kellie L.
Pavlova, Maria N.
Vassilatis, Demetri
Zeng, Hongkui

<120> G PROTEIN COUPLED RECEPTORS AND USES THEREOF

<130> 700128.401USPC

<140> 10527265
<141> 2007-11-15

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<170> PatentIn version 3.3

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<213> Homo sapiens

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35 40 45

Ser Arg Lys Gly Arg His Thr Leu Leu Asn Phe Cys Phe His Ala Ala
50 55 60

Leu Thr Phe Thr Val Phe Ala Gly Gly Ile Asn Arg Thr Lys Tyr Pro
65 70 75 80

Ile Leu Cys Gln Ala Val Gly Ile Val Leu His Tyr Ser Thr Leu Ser
85 90 95

Thr Met Leu Trp Ile Gly Val Thr Ala Arg Asn Ile Tyr Lys Gln Val
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Thr Lys Lys Ala Pro Leu Cys Leu Asp Thr Asp Gln Pro Pro Tyr Pro
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Arg Gln Pro Leu Leu Arg Phe Tyr Leu Val Ser Gly Gly Val Pro Phe
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Ile Ile Cys Gly Val Thr Ala Ala Thr Asn Ile Arg Asn Tyr Gly Thr
145 150 155 160

Glu Asp Glu Asp Thr Ala Tyr Cys Trp Met Ala Trp Glu Pro Ser Leu
165 170 175

Gly Ala Phe Tyr Gly Pro Ala Ala Ile Ile Thr Leu Val Thr Cys Val
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Tyr Phe Leu Gly Thr Tyr Val Gln Leu Arg Arg His Pro Gly Arg Arg
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Tyr Glu Leu Arg Thr Gln Pro Glu Glu Gln Arg Arg Leu Ala Thr Pro
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Glu Gly Gly Arg Gly Ile Arg Pro Gly Thr Pro Pro Ala His Asp Ala
225 230 235 240

Pro Gly Ala Ser Val Leu Gln Asn Glu His Ser Phe Gln Ala Gln Leu
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Arg Ala Ala Ala Phe Thr Leu Phe Leu Phe Thr Ala Thr Trp Ala Phe
260 265 270

Gly Ala Leu Ala Val Ser Gln Gly His Phe Leu Asp Met Val Phe Ser
275 280 285

Cys Leu Tyr Gly Ala Phe Cys Val Thr Leu Gly Leu Phe Val Leu Ile
290 295 300

His His Cys Ala Lys Arg Glu Asp Val Trp Gln Cys Trp Trp Ala Cys
305 310 315 320

Cys Pro Pro Arg Lys Asp Ala His Pro Ala Leu Asp Ala Asn Gly Ala

325 330 335

Ala Leu Gly Arg Ala Ala Cys Leu His Ser Pro Gly Leu Gly Gln Pro
340 345 350

Arg Gly Phe Ala His Pro Pro Gly Pro Cys Lys Met Thr Asn Leu Gln
355 360 365

Ala Ala Gln Gly His Ala Ser Cys Leu Ser Pro Ala Thr Pro Cys Cys
370 375 380

Ala Lys Met His Cys Glu Pro Leu Thr Ala Asp Glu Ala His Val His
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Leu Gln Glu Glu Gly Ala Phe Gly His Asp Pro His Leu His Gly Cys
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Leu Gln Gly Arg Thr Lys Pro Pro Tyr Phe Ser Arg His Pro Ala Glu
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Glu Pro Glu Tyr Ala Tyr His Ile Pro Ser Ser Leu Asp Gly Ser Pro
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Arg Ser Ser Arg Thr Asp Ser Pro Pro Ser Ser Leu Asp Gly Pro Ala
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Gly Thr His Thr Leu Ala Cys Cys Thr Gln Gly Asp Pro Phe Pro Met
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Val Thr Gln Pro Glu Gly Ser Asp Gly Ser Pro Ala Leu Tyr Ser Cys
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Pro Thr Gln Pro Gly Arg Glu Ala Ala Leu Gly Pro Gly His Leu Glu
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Met Leu Arg Arg Thr Gln Ser Leu Pro Phe Gly Gly Pro Ser Gln Asn
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35 40 45

Ile Arg Ile Ser Arg Lys Gly Arg His Ala Leu Leu Asn Phe Cys Phe
50 55 60

His Ala Ala Leu Thr Phe Thr Val Phe Ala Gly Gly Ile Asn Arg Thr
65 70 75 80

Gln His Pro Ile Leu Cys Gln Ala Val Gly Ile Ala Leu His Tyr Ser
85 90 95

Thr Leu Ser Thr Met Leu Trp Ile Gly Val Thr Ala Arg Asn Ile Tyr
 100 105 110

Lys Gln Val Thr Lys Lys Ala Leu Pro Cys Pro Gly Ala Asp Gln Pro
115 120 125

Pro Tyr Pro Lys Gln Pro Leu Leu Arg Phe Tyr Leu Ile Ser Gly Gly
130 135 140

Val Pro Phe Ile Ile Cys Gly Val Thr Ala Ala Thr Asn Ile Arg Asn
145 150 155 160

Tyr Gly Thr Glu Asp Glu Asp Val Ala Tyr Cys Trp Met Ala Trp Glu
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Pro Ser Leu Gly Ala Phe Tyr Gly Pro Ala Ala Phe Ile Ala Leu Val
180 185 190

Thr Cys Val Tyr Phe Leu Cys Thr Tyr Val Gln Leu Arg Arg His Pro
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Glu Arg Arg Tyr Glu Leu Arg Glu Arg Thr Glu Glu Gln Gln Arg Leu
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Pro Thr Cys Asp Ala Leu Ala Ala Ser Gln Leu Gln Asn Glu His Ser
245 250 255

Phe Lys Ala Gln Leu Arg Ala Ala Phe Thr Leu Phe Leu Phe Thr
260 265 270

Ala Thr Trp Thr Phe Gly Ala Leu Ala Val Ser Gln Gly His Phe Leu
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Asp Met Ile Phe Ser Cys Leu Tyr Gly Ala Phe Cys Val Thr Leu Gly
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Leu Phe Val Leu Ile His His Cys Ala Lys Arg Glu Asp Val Trp Gln
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Cys Trp Trp Ser Cys Cys Pro Ser Arg Gly Asp Thr Ser Thr Thr Lys
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Thr Ala Cys Leu Gln Asp Ser Pro Cys Pro Gly Lys Leu Arg Gly Phe
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Gly His Pro Pro Ala Ser His Cys Lys Met Thr Asn Leu Gln Ala Ala
370 375 380

Gln Gly His Val Ser Cys Leu Ser Pro Ala Thr Pro Cys Cys Ala Lys
385 390 395 400

Met His Cys Glu Gln Leu Met Glu Glu Ala Ala His Ile His Met
405 410 415

Ala Glu Glu Asp Val Tyr Pro His Asp Pro His Leu His Asp Pro His
420 425 430

Leu His Arg Cys Leu Lys Gly Arg Thr Lys Ser His Tyr Phe Ser Arg
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His Gln Ala Ala Ala Ala Glu Arg Glu Tyr Ala Tyr His Ile Pro Ser
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Ser Leu Glu Gly Pro Met Gly Met His Thr Leu Ala Cys Cys Ala Gln
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Ala Asp Pro Phe Pro Met Val Ser Gln Pro Glu Gly Asp Thr Ser
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Pro Gly Leu Tyr Gly Cys Pro Pro His Leu Ser Pro Gly Pro Ala His
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Leu Glu Met Leu Arg Arg Thr Gln Ser Leu Pro Phe Gly Gly Pro Ser
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Gln Asn Gly Leu Leu Gln Gly Asp Val Arg Glu Gly Leu Pro Phe Gly
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Asn Ile Tyr Leu Phe Cys Leu Thr Cys Leu Met Thr Phe Ala Ala Leu		
35	40	45

Val Gly Ser Ile Tyr Ser Leu Ile Ser Leu Leu Lys Met Gln Asn Arg		
50	55	60

Thr Val Val Ser Met Leu Val Ala Ser Trp Ser Val Asp Asp Leu Met			
65	70	75	80

Ser Val Leu Ser Val Thr Ile Phe Met Phe Leu Gln Trp Pro Asn Glu		
85	90	95

Val Pro Gly Tyr Phe Gln Phe Leu Cys Thr Thr Ser Ala Leu Met Tyr
100 105 110

Leu Cys Gln Gly Leu Ser Ser Asn Leu Lys Ala Thr Leu Leu Val Ser
115 120 125

Tyr Asn Phe Tyr Thr Met His Arg Gly Val Gly Ser Gln Thr Ala Ser
130 135 140

Arg Arg Ser Gly Gln Val Leu Gly Val Val Leu Thr Val Trp Ala Ala
145 150 155 160

Ser Leu Leu Leu Ser Ala Leu Pro Leu Cys Gly Trp Gly Ala Phe Val
165 170 175

Arg Thr Pro Trp Gly Cys Leu Val Asp Cys Ser Ser Ser Tyr Val Leu
180 185 190

Phe Leu Ser Ile Val Tyr Ala Leu Ala Phe Gly Leu Leu Val Gly Leu
195 200 205

Ser Val Pro Leu Thr His Arg Leu Leu Cys Ser Glu Glu Pro Pro Arg
210 215 220

Leu His Ser Asn Tyr Gln Glu Ile Ser Arg Gly Ala Ser Ile Pro Gly
225